



SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
Uses Related Thereto

(iii) NUMBER OF SEQUENCES: 35

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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPad

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/016,869
(B) FILING DATE: 30-JAN-1998

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/893,274
(B) FILING DATE: 15-JUL-1994

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/306,511
(B) FILING DATE: 14-SEP-1994

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/248,812
(B) FILING DATE: 25-MAY-1994

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/227,371
(B) FILING DATE: 14-APR-1994

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/154,915
(B) FILING DATE: 18-NOV-1993

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/991,997
(B) FILING DATE: 17-DEC-1992

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(C) REFERENCE/DOCKET NUMBER: GPCI-P10-071

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 994 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 41..508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATG GAT CCG GCG GCG	55
Met Asp Pro Ala Ala	
1 5	
GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC ACG GCC GCG GCG	103
Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala	
10 15 20	
CGG GGT CGG GTA GAG GAG GTG CGG GCG CTG CTG GAG GCG GTG GCG CTG	151
Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu	
25 30 35	
CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG	199
Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met	
40 45 50	
ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTC CAC GGC GCG GAG	247
Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu	
55 60 65	
CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC GTG CAC GAC GCT	295
Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala	
70 75 80 85	
GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG	343
Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly	
90 95 100	
GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG	391
Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu	
105 110 115	
GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT	439
Ala Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala	
120 125 130	
GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA	487
Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu	
135 140 145	
GGT CCC TCA GAC ATC CCC GAT TGAAAGAACCC AGAGAGGCTC TGAGAACCT	538
Gly Pro Ser Asp Ile Pro Asp	
150 155	
CGGGAAACTT AGATCATCAG TCACCGAAGG TCCTACAGGG CCACAACTGC CCCCAGCCACA	598
ACCCACCCCG CTTTCGTAGT TTTCATTAG AAAATAGAGC TTTTAAAAAT GTCTGCCTT	658
TTAACGTAGA TATAAGCCTT CCCCCACTAC CGTAAATGTC CATTATATC ATTTTTATA	718
TATTCTTATA AAAATGTAAA AAAGAAAAAC ACCGCTCTG CCTTTCACT GTGTTGGAGT	778
TTTCTGGAGT GAGCACTCAC GCCCTAACCG CACATTATG TGGGCATTTC TTGCGAGCCT	838
CGCAGCCTCC GGAAGCTGTC GACTTCATGA CAAGCATTG GTGAACTAGG GAAGCTCAGG	898
GGGGTTACTG GCTTCTCTG AGTCACACTG CTAGCAAATG GCAGAACCAA AGCTCAAATA	958

AAAAATAAAAT TATTTTCATT CATTCACTCA AAAAAAA

994

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
1 5 10 15
Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
20 25 30
Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
35 40 45
Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
50 55 60
Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
65 70 75 80
Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
85 90 95
Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
100 105 110
Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
115 120 125
Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
130 135 140
Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 328..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGGACTCCG CGACGGTCCG CACCTGCGG CCAGAGCGGC	TTTGAGCTCG GCTGCCTCCG	60
CGCTAGGCGC TTTTCCAG AAGCAATCCA GGCAGCGCCG	CTGGTTCTTG AGGCCAGGA	120
AAAGCCCGGA GCTAACGACC GGCCGCTCGG CACTGCACGG	GGCCCCAAGC CGCAGAAGAA	180
GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCCTA	GGAAGGAGAG AGTGCGCCGG	240
AGCAGCGTGG GAAAGAAGGG AAGAGTGTG	TTAAGTTTAC GGCCAACGGT GGATTATCCG	300
GGCCGCTGCG CGTCTGGGG CTGCGGA ATG CGC GAG AAC AAG GGC ATG		351
	Met Arg Glu Asn Lys Gly Met	
	1 5	
CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA		399
Pro Ser Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly		
10 15 20		
CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC		447

Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn	
25 30 35 40	
GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC	495
Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly	
45 50 55	
AGC GCC CGC GTG GCG GAG CTG CTG CTC CAC GGC GCG GAG CCC AAC	543
Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu Pro Asn	
60 65 70	
TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCC CGG	591
Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg	
75 80 85	
GAG GGC TTC CTG GAC ACG CTG GTG CTG CAC CGG GCC GGG GCG CGG	639
Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg	
90 95 100	
CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG	687
Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu	
105 110 115 120	
GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG	735
Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly	
125 130 135	
GAC TGACGCCAGG TTCCCCAGCC GCCCACAAACG ACTTTATTTT CTTACCCAAT	788
Asp	
TTCCCCACCCCC CACCCACCTA ATTGATGAA GGCTGCCAAC GGGGAGCGG	837

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Ser Asp Glu	
1 5 10 15	
Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser	
20 25 30	
Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg	
35 40 45	
Ala Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu	
50 55 60	
Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr	
65 70 75 80	
Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val	
85 90 95	
Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly	
100 105 110	
Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala	
115 120 125	
Gly Tyr Leu Arg Thr Ala Thr Gly Asp	
130 135	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 213..587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAGTACAGC AGCGGGAGCA TGGGTCGCAG GTTCTGGTC ACTGTAAGGA TTCAGCGCGC	60
GGGCCGCCCA CTCCAAGAGA GGGTTTCTT GGTGAAGTTC GTGCGATCCC GGAGACCCAG	120
GACAGCGAGC TGCGCTCTGG CTTTCGTGAA CATGTTGTTG AGGCTAGAGA GGATCTTGAG	180
AAGAGGGCCG CACCGGAATC CTGGACCAGG TG ATG ATG ATG GGC AAC GTT CAC	233
Met Met Met Gly Asn Val His	
1 5	
GTA GCA GCT CTT CTG CTC AAC TAC GGT GCA GAT TCG AAC TGC GAG GAC	281
Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp	
10 15 20	
CCC ACT ACC TTC TCC CGC CCG GTG CAC GAC GCA GCG CGG GAA GGC TTC	329
Pro Thr Thr Phe Ser Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe	
25 30 35	
CTG GAC ACG CTG GTG GTG CTG CAC GGG TCA GGG GCT CGG CTG GAT GTG	377
Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala Arg Leu Asp Val	
40 45 50 55	
CGC GAT GCC TGG GGT CGC CTG CCG CTC GAC TTG GCC CAA GAG CGG GGA	425
Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln Glu Arg Gly	
60 65 70	
CAT CAA GAC ATC GTG CGA TAT TTG CGT TCC GCT GGG TGC TCT TTG TGT	473
His Gln Asp Ile Val Arg Tyr Leu Arg Ser Ala Gly Cys Ser Leu Cys	
75 80 85	
TCC GCT GGG TGG TCT TTG TGT ACC GCT GGG AAC GTC GCC CAG ACC GAC	521
Ser Ala Gly Trp Ser Leu Cys Thr Ala Gly Asn Val Ala Gln Thr Asp	
90 95 100	
GGG CAT AGC TTC AGC TCA AGC ACG CCC AGG GCC CTG GAA CTT CGC GGC	569
Gly His Ser Phe Ser Ser Thr Pro Arg Ala Leu Glu Leu Arg Gly	
105 110 115	
CAA TCC CAA GAG CAG AGC TAAATCCGCC TCAGCCGCC TTTTTCTTCT	617
Gln Ser Gln Glu Gln Ser	
120 125	
TAGCTTCACT TCTAGCGATG CTAGCGTGTG TAGCATGTGG CTTTAAAAAA TACATAATAA	677
TGCTTTTTT GCAATCACGG GAGGGAGCAG AGGGAGGGAG CAGAAGGAGG GAGGGAGGGA	737
GGGAGGGACC TGGACAGGAA AGGAATGGCA TGAGAAACTG AGCGAAGGCG GCCCGAAGG	797
GAATAATGGC TGGATTGTTT AAAAAATAA AATAAAGATA CTTTTAAAAA TGTCAA	853

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly
1 5 10 15

Ala Asp Ser Asn Cys Glu Asp Pro Thr Thr Phe Ser Arg Pro Val His
20 25 30

Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly
35 40 45

Ser Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu
50 55 60

Asp Leu Ala Gln Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg
65 70 75 80

Ser Ala Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys Thr Ala
85 90 95

Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Thr Pro
100 105 110

Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCA CTC CTG GAA GCC GGC GCA GAT CCC AAC GCC CTG AAC CGC TTC GGG 48
Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly
1 5 10 15

AGG CGC CCA ATC CAG GTC ATG ATG GGC AGC GCC AGG GTG GCA GAG 96
Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu
20 25 30

CTG CTG CTG CTC CAC GGA GCA GAA CCC AAC TGC GCC GAC CCT GCC ACC 144
Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr
35 40 45

CTT ACC AGA CCT GTG CAC GAC GCA GCT CGG GAA GGC TTC CTG GAC ACG 192

Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr
50 55 60
CTT GTC GTG CTG CAC CGG GCA GGG GCG CGG TTG GAT GTG
Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val
65 70 75

231

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly
1 5 10 15

Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu
20 25 30

Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr
35 40 45

Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr
50 55 60

Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala
1 5 10 15

Tyr Gly Thr Val Tyr Lys Ala Xaa Asp Pro His Ser Gly His Phe Val
20 25 30

Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly
35 40 45

Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
50 55 60

Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
65 70 75 80

Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val
85 90 95

Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu
100 105 110

Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu
115 120 125

Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu
130 135 140

Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly
145 150 155 160

Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val
165 170 175

Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala
180 185 190

Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe
195 200 205

Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly
210 215 220

Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg
225 230 235 240

Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro
245 250 255

Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu
260 265 270

Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg
275 280 285

Ala Leu Gln His Ser Tyr Leu His Lys Asp Glu Gly Asn Pro Glu
290 295 300

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Glu Lys Asp Gly Leu Cys Arg Ala Asp Gln Gln Tyr Glu Cys Val
1 5 10 15

Ala Glu Ile Gly Glu Gly Ala Tyr Gly Lys Val Phe Lys Ala Xaa Asp

20	25	30
Leu Lys Asn Gly Gly Arg Phe Val Ala Leu Lys Arg Val Arg Val Gln		
35	40	45
Thr Gly Glu Glu Gly Met Pro Leu Ser Thr Ile Arg Glu Val Ala Val		
50	55	60
Leu Arg His Leu Glu Thr Phe Glu His Pro Asn Val Val Arg Leu Phe		
65	70	75
Asp Val Cys Thr Val Ser Arg Thr Asp Arg Glu Thr Lys Leu Thr Leu		
85	90	95
Val Phe Glu His Val Asp Gln Asp Leu Thr Thr Tyr Leu Asp Lys Val		
100	105	110
Pro Glu Pro Gly Val Pro Thr Glu Thr Ile Lys Asp Met Met Phe Gln		
115	120	125
Leu Leu Arg Gly Leu Asp Phe Leu His Ser His Arg Val Val His Arg		
130	135	140
Asp Leu Lys Pro Gln Asn Ile Leu Val Thr Ser Ser Gly Gln Ile Lys		
145	150	155
160		
Leu Ala Asp Phe Gly Leu Ala Arg Ile Tyr Ser Phe Gln Met Ala Leu		
165	170	175
Thr Ser Val Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu		
180	185	190
Gln Ser Ser Tyr Ala Thr Pro Val Asp Leu Trp Ser Val Gly Cys Ile		
195	200	205
Phe Ala Glu Met Phe Arg Arg Lys Pro Leu Phe Arg Gly Ser Ser Asp		
210	215	220
Val Asp Gln Leu Gly Lys Ile Leu Asp Val Ile Gly Leu Pro Gly Glu		
225	230	235
240		
Glu Asp Trp Pro Arg Asp Val Ala Leu Pro Arg Gln Ala Phe His Ser		
245	250	255
Lys Ser Ala Gln Pro Ile Glu Lys Phe Val Thr Asp Ile Asp Glu Leu		
260	265	270
Gly Lys Asp Leu Leu Lys Cys Leu Thr Phe Asn Pro Ala Lys Arg		
275	280	285
Ile Ser Ala Tyr Ser Ala Leu Ser His Pro Tyr Phe Gln Asp Leu Glu		
290	295	300
Arg Cys Lys Glu Asn Leu Asp Ser His Leu Pro Pro Ser Gln Asn Thr		
305	310	315
320		
Ser Glu Leu Asn Thr Ala		
325		

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly
1 5 10 15

Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
35 40 45

Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
50 55 60

Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu
65 70 75 80

Arg Xaa Ala Xaa Gly
85

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
1 5 10 15

Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
20 25 30

Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
35 40 45

Ile Gln Val Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu
50 55 60

Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa
65 70 75 80

Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
85 90 95

Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
100 105 110

Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa
115 120 125

Xaa Tyr Leu Arg Xaa Ala Xaa Gly Gly Thr Arg Gly Ser Asn His Ala
130 135 140

Arg Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Ser Asp Glu
1 5 10 15

Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
20 25 30

Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
35 40 45

Ala Ile Gln Val Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu
50 55 60

Leu Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa
65 70 75 80

Xaa Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu
85 90 95

Val Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp
100 105 110

Gly Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa
115 120 125

Xaa Xaa Tyr Leu Arg Xaa Ala Xaa Gly Asp
130 135

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly
1 5 10 15

Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
35 40 45

Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
50 55 60

Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu
65 70 75 80

Arg Xaa Ala Xaa Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys
85 90 95

Thr Ala Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser
100 105 110

Thr Pro Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Ala Glu Ile Gly Xaa Gly Ala Tyr Gly Xaa Val Xaa Lys Ala Arg Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Xaa Lys Ala Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ala Arg Asp
1

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 960 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGAGAGGGA ATT CGGCACGA GGCAGCATG GAGCCTTCGG CTGACTGGCT GGCCACGGCC	60
CGGGCCCGGG GTCGGGTAGA GGAGGTGCGG GCGCTGCTGG AGGCGGTGGC GCTGCCCAA	120
CGCACCGAAT AGTTACGGTC GGAGGCCGAT CCAGGTCATG GATGATGGC AGCGCCCCGA	180
GTGGCGGAGC TGCTGCTGCT CCACGGCGCG GAGCCAACT GCGCCGACCC CGCCACTCTC	240

ACCCGACCCG TGCACCACGC TGCCCAGGAG GGCTTCTGGA CACGCTGGTG GTGCTGCACC	300
GGGCCGGGGC GCGGCTGGAC GTGCGCGATG CCTGGGGCCG TCTGCCGTG GACCTGGCTG	360
AGGAGCTGGG CCATCGCGAT GTCGCACGGT ACCTGCGCGC CCGTGCAGGG GGCACCAAGAG	420
GCAGTAACCA TGCCCGATA GATGCCGCAGG AAGGTCCCTC AGACATCCCC GATTGAAAGA	480
ACCAGAGAGG CTCTGAGAAA CCTCGGGAAA CTTAGATCAT CAGTCACCGA AGGTCCCTACA	540
GGGCCACAAC TGCCCCGCC ACAACCCACC CCGCTTCGT AGTTTCATT TAGAAAATAG	600
AGCTTTAAA AATGTCTGC CTTTAACGT AGATATAAGC CTTCCCCAC TACCGTAAAT	660
GTCCATTTAT ATCATTTTT ATATATTCTT ATAAAAATGT AAAAAAAGAA AACACCGCT	720
TCTGCCTTT CACTGTGTTG GAGTTTCTG GAGTGAGCAC TCACGCCCTA AGCGCACATT	780
CATGTGGCA TTTCTGCGA GCCTCGCAGC CTCCGGAAGC TGTCGACTTC ATGACAAGCA	840
TTTGTGAAC TAGGAAAGCT CAGGGGGTT ACTGGCTTCT CTTGAGTCAC ACTGCTAGCA	900
AATGGCAGAA CCAAAGCTCA AATAAAAATA AAATTATTTC CATTCAATTCA CTCAAAAAAA	960

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGNGGNAAGN TGTGGGGAA AGTTTGGGGA TGGAANACCA ANCCCTCCCT TCNTTACCAA	60
ACNCTGGCTC TGNCGAGGCT NCNTCCGANT GGTNCCCCG GGGGAGACCC AACCTGGGNC	120
GACTTCAGGG NTGCNACATT CATTCACTAA GTGCTNGGAG NTAATANCAC CTCCTCCGAG	180
CANNGACAGG NTCGGAGGGG GCTCTTCCCC CANCACCGA GGAAGAAAGA GGAGGGNCTN	240
CGGAGAGGGG GAGAACAGAC AACGGCGGC GGGGAGCAGC ATGGATCCGG CGGCGGGGAG	300
CAGCATGGAN CCTTCGACTG ACTGACTGCC TCGC	334

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCNCTTATTG NTAGGANATA ATAACACCTC CACCGATAAC TTCACTTACA ACGTCCCNNT	60
TCCTGGAAAG ATACACAGCG TTCCCTCCAG AGGATTGTG GGACAGGGTN GGAGNGGTCT	120
CTTCCNCCAC CACCGGAGGA AGAAAGAGGA GGGGCTGNCT GTTCACCAGA GGGTGGGACG	180
GACCNCGTAC GCTCGNCGNC TNCGGAGAGG GGGAGAGCAT CANCGGNCGN CGGGGAGCAA	240
CATGGAACCG NCGGCGGGGA GCAGCATGGA NCCTTCGGCT GACTGGCTGN CCACGNCCAC	300
GNCCCGGGGT CGGGTAGAGG AGGTGCGGNC GCTNCTGGAG GCGGGGNCTC TGNCCAACNC	360
GCTAAAAN	368

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACNNNCTCC GGCCGGNGTC GGGTAGAGGA GGTGCGGGCG CTGCTGGAGG CGGGGGCGCT	60
GCCCAACGCA CCGAATAGTT ACGGTCGGAG GCCGATCCAG GTNNGGGTAG AGGGTCTGCA	120
GCGGGAGCAG GGGATGGCGG GCGACTCTGG AGGACGAAGT TTGCAGGGGA ATTGGAATCA	180
GGTAGCGCTT CGATTCTCCN GAAAAAGGGG AGGCTTCCTG GGGAGTTTC AGAAGGGTT	240
TGTAATCACA GACCTCCTCC TGGCGACGTC CTGGGGGCTT GGGAAAGCAA GGAAGAGGAA	300
TNAGGAGCCA CGCGCGTACG AGTCTCTCGA ATGCTGAGAA GATCTNAAGG GGGAACATA	360
TTTGTATTAG CNTCCAAGTN TNCTCTNTAT CANATACAAA NTNC	404

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCTNANCCC GGGTAGAGGG TCTGCAGCGG GAGCAGNGGA TGGCGGGCGA CTCTGGAGGA	60
CGAAGTTGGC AGGGGAATTG GAATCAGGTA GCGCTTCGAN TCTCCGGAAA AAGGGGAGGC	120
TTCCTGGGA GTTNNCAGAA GGGGTTTGTG ATCACAGNCC TCCNCCTGGC GACGCCCTGG	180
GGGGTTGGGA AGCCAAGGAA GAGGAATGAG GAGNCACGCG CNTACAGNTC TCTCGAATNC	240
TGANAAGATC TGAAGGGGG AACATATTTG TATTAGNATN NAAGTATGCT CTTTATCAGA	300
TAGAAAATTC ACGAACGTGT GGNATAAAA GGGAGTCTTA AAGAAATNTA AGATGTGCTG	360
GGACTACTTA GCCTCCAANA CACAGATNCC TGGATGGAGC T	401

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAAANNAAAA AAAATCTCCC AGGCCTAACAA TAATTNTCAG GAAAGAAATT TCAGTAGTTG	60
NATCTCAGGG GAAATACAGG AAGTTAGCCT GGAGTAAAAG TCAGTGTGTC CCTGCCCTT	120
TGCTANATTG CCCGTGCCTC ACAGTGCTCT CTGCCTGTGA CGACAGCTCC NCAGAAGTTC	180
GGAGGATATA ATGGAATTCA TTGTGTACTG AAGAATGGAT AGAGAACTCA AGAAGGAAAT	240
TGGAAACTGG AAGCAAATGT AGGGGTAATT AGACACCTGG GGCTTCTGTG GGGGTCTGCT	300
TGGCGGTGAG GGGGCTCTAC ACAAGCTTCC TTTCCGTCAT GCCGNCCCC ACCCTGGCTC	360
TGACCATTCT GTTCTCTCTG GCAGGTCATG ATGATGGCA GCGCCCGAGG CGCGGAGCTG	420
CTGCTGCTCC ACGGCGCGGA GCCCACTGCT CCGACGCCG	459

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AANAAAAAAG AAATNGATAA NATAGAGGAA TGAACANATT AAAATCAAAA AACANAACAN	60
AGACATAATA AAAAACGAGA ATGTTCTAGA CNTAACATCA ATTATAAAGC TCAAGACTCA	120
TTGATATNAA GGADATTGAA GGGAAATCTT AACTAGCACA ANNGNATNAA AAAANAATTC	180
CCACGACACC GCCACTCTCA ACGCATCCGT GCTCGACACT GCCCGGGAGG TCNTCCTGGA	240
CACGCTGGTG GTNCTCCACC GGNCCGGGGC ACGTCTGGAC GTGCGCGATG CCTGGGNCCG	300
NCTACCCGTG GTACCTGACT GAGGACCTGG GCCATCCCGA TTTCGCNNGG TANCTCNNGN	360
GGCTGNGGGG GCCAANAGAG GNCANTACCC	390

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCTGCNACGA CCCC GCCACT CTCACCCGAC CCGTGCACGA CGCTGTCCGG GAGGGTTTCC	60
TGGACACGCT GGTGGTGCTG CACC GGGCCG GGGNGCGGTT GGACGTGCGC GATGCCTGGG	120
GCCGCCTNCC CGTGGNACCT GGTTGAGGAG CTGGGNACATC GCGATGTCGC ACGGTACCTG	180
CGCGCGTTGC GGGGGCACC AGAGGNNAGT NACC	214

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

NCTCTCACGG TGGGGAGGCC AACTGCGCCG AACCCGCCAC TCTCACCCGA CCCGCGCACG	60
ACGGTGCCCG GGAGGGGTTTC CTGGACACGC TGGTGGTGCT GCACCGGGCC GGGGCGCGGC	120
TGGACGTTCG NGATGCCTGG GGGNTCTNTC CGTNGNACCT GGCTGAAGAG CTGGNNACATC	180
GNGATGTCGC ACGGCCNCTG TGTGNGGNTG CGGGGGCAC CATAGGTCAG TNTCC	235

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

NAAGTATGAG CGAACNAAT TGTGGTTGAA GAANAGGAA TCGTAGGGAA CTTCGGGATC	60
CCNCNGGGAN CNCCAGAACCC TGAGNCGCCN ATTGGAAATN ACAAACTGNC TGNATCACTC	120
CGNACCAGGT NCAAAAGATA CCTGGGGANG CGGGAAAGGGA AAGACNACAT CNAGACCGCC	180
TTCGCNCCTN GGNATTGTGA GCAGCCTCTG AGACTCATTN ATATNACACT CTCGTNTTC	240
TTCTTACAAC CCTGCAGNCC GCGCGGTGCG GCTTCTCTG CCCTCCGCCG GGTGGACCTG	300
GAGCGCTTGA GCGGTCGGCG CGCCTGGAGC AGCCAGGCAG NCAGTGGACT AGCTGCTGGA	360
CCAGGGAGGT GTGGGAGAGC GGTGGCGGCG GGTACATGCA CGTGAAGCCA TTGCGAGAAC	420
TTTATCCATA AGTATTCAA TACCGGTAGG GACGGCAAGA GAGGAGGGCG GGATGTGCCA	480
CACATCTTG ACCTCAGGTT TCTAACGCCT GTTTCTTTC TGCCCTCTGC AGACAACCCC	540
CGATTGAAAG AACCAAGAGAG GCTCTGAGAA ACC	573

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCCCATCGCG CCTTGGGANT GTGAGCNACC ATTGAGACTC ATNAATATAG CACTCGTTT	60
TCTTCTTGCA ACCCTGCCCN CCGCGCGGTC GCGCTNTCTC TGCCCTCCGC NGGGTGGACC	120
TGGAGCGAGC GCTTGAGCGG TCGGTGGCGG CNCCCTGGANC AGCCAGGCAG GCAGTGGACT	180
ACCTNCTGGA CCAGGGACCT GTGGGAGAGC GGTGNCGGCG GGTACATGCA CGTGAAGCCA	240
TTGCGAGAAC TTTATCCATA AGTATTCAA TGCCGGTAGG GACGGCAAGA GAGGAGGGCG	300

GGATGTNCCA CACATCTTG ACCTCAGGTT TCTAACGCCT GTTTCTTTC TGCCCTCTGC	360
AGACATCCCC GATTGAAAGA ACCAGAGAGG CTCTGAGAAA CCTCCGGAAA CTTAGNTCAT	420
CANTCGCCGN AAAA	434

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGAAATTAGA TCATCAGTCA CCGATCCTCC TACAGGGNCA CAACTGNCCC CGCCACAAACC	60
CACCCCGNTT TCGTAGTTTT CATTAGAAA ATAGAGCTTT TAAAAATGTC CTGCCTTTA	120
ACGTAGATAT ATGCCTTCCC CCACTACCGN AAATGTCCAT TTATATCATN TTTTATATAT	180
TCTTATAAAA ATGTAAAAAA GAAAAACACC GCTTCTGCCT TTTCACTGTG TTGGAGTTTT	240
CTGGAGTGAG CACTCACGCC CTAAGCGCAC ATTCACTGTGG GCATTTCTTG CGAGCCTCGC	300
AGNCTCCGGA AGCTGTCGAC CTCGAGGGGG GGNCCGGTAC CCAATTGCC CTATAGTGAG	360
TCGTATTACA ATTCACTGGN CGNCGNTTT ACAACGTCGG TGGACTGGGA AAACCCCGGN	420
GTTACCCAAC TTTAATCGNC TTGGAGGACA TCCCCCTTT CGCCAGNTGG GGTTATAGNG	480
AAGAGGGCCN CACCNNTCGC CC	502

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CANCNATNTN CGGCATTTCT NGNGAGCCTC GTAGTCTCCG GATGNTGTCG ACCTCGAGGG	60
GGGGNCCNGT ACCCAATTG NCCTATNGTG AGTCGTNTTA CAATTCACTG GCCGCCGTTT	120
TNACAACGTC GNTGNACTGG GAAAACCTG GTGTTACCCA ACTTNAATGT CCTTGNAGNA	180
CATCCCCCTT TNCGCCAGCT GGTGTAATAG CGANGAGGCC CGCACCGATC GCCCTTCCCA	240

ACAGTTGNGC AGCCTGAATG GCGAATGGAA ATTGTAAGCG TTAATATTT GTTAAAATTC	300
GCGTTANATC NTCGGTTAAN TCAGCTCATN TTTTATCCAA TAGGCCGANA TCGGCANAAT	360
CCCCAATAAA TCAANAGAAT AGACCGAGAT AGGGTTGAGT GTCGTTCCAG TTNGGGAACA	420
NGAGTCCACT ATTAAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAACC NTNTTCAGN	480
GGATTGGNCC ACTACGCNTA NCC	503

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 515 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CANCNATNTN CGGCATTTCT NGNGAGCCTC GTAGTCTCCG GATGNTGTCG ACCTCGAGGG	60
GGGGNCCNGT ACCCAATTG NCCTATNGTG AGTCGTNTTA CAATTCACTG GCCGCCGTTT	120
TNACAACGTC GNTGNACTGG GAAAACCTG GTGTTACCCA ACTTNAATCG CCTTGNAGNA	180
CATCCCCCTT TNCGCCAGCT GGTGTAATAG CGANGAGGCC CGCACCGATC GCCCTTCCCA	240
ACAGTTGNGC AGCCTGAATG GCGAATGGAA ATTGTAAGCG TTAATATTT GTTAAAATTC	300
GCGTTANATC NTCGGTTAAN TCAGCTCATN TTTTATCCAA TAGGCCGANA TCGGCANAAT	360
CCCCAATAAA TCAANAGAAT AGACCGAGAT AGGGTTGAGT GTCGTTCCAG TTNGGGAACA	420
NGAGTCCACT ATTAAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAACC NTNTTCAGN	480
GGATTGGNCC ACTACGCNTA NCCATCACCC TATTC	515

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
1 5 10 15

His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
35 40 45 50

Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
55 60 65

Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala
70 75 80 85

Ala Gly Gly Thr

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
1 5 10 15

His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
35 40 45 50

Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
55 60 65

Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala
70 75 80 85

Thr Gly Asp

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala
1 5 10 15

Asp Ser Asn Cys Glu Asp Pro Thr Thr Phe Ser Arg Pro Val His Asp Ala
20 25 30

Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala
35 40 45 50

Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln
55 60 65

Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg Ser Ala Gly Cys Ser
70 75 80 85

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala Arg Gly Arg
1 5 10 15

Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu Pro Asn Ala
20 25 30

Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met Met Gly Ser
35 40 45

Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu Pro Asn Cys
50 55 60

Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu
65 70 75 80

Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg Leu
85 90 95

Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Glu
100 105 110

Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala Ala Gly Gly
115 120 125

Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu Gly Pro Ser
130 135 140

Asp Ile Pro Asp
145